

In the Sequence Listing:

Please insert a paper copy of the sequence listing as new pages 1-49 in the above-mentioned application.



SEQUENCE LISTING

<110> Snutch, Terrance
Baillie, David L.

<120> MAMMALIAN T-TYPE CALCIUM CHANNELS

<130> 38109-20007.21

<140> 09/611,257
<141> 2000-07-06

<150> 09/346,794
<151> 1999-07-02

<150> 09/030,428
<151> 1998-02-25

<150> 60/039,204
<151> 1997-02-28

<160> 49

<170> FastSEQ for Windows Version 4.0

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24

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<400> 3

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<210> 4
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<211> 24
<212> DNA
<213> Artificial Sequence

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<223> oligonucleotide probe for locating calcium channel

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a6
CMT

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<212> DNA
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<223> oligonucleotide probe for locating calcium channel

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<210> 8
<211> 24
<212> DNA
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<211> 168
<212> DNA
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cttcccagag tgagctcatc cacctcgatc tgcctgactc gacgttca 168

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<212> DNA

<213> Homo sapiens

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<211> 94

<212> DNA

<213> Homo sapiens

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<211> 123

<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 Gly Lys Tyr Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile
 35 40 45
 Gln Ala Leu Lys Gln Leu Met Phe Lys Leu Val Ala Thr Val Ala Arg
 50 55 60
 Thr His Ala Thr Pro Ser His Ile Thr Gly Gly Pro Gly Thr Gly Met
 65 70 75 80
 His Thr Gly Thr Phe Gln Glu Gly Ala Glu Pro Gly Ser Ser Gln His
 85 90 95
 Pro Glu Ala Gln Ala Thr Tyr Thr Ala Gly Cys Thr Pro Ala Pro Thr
 100 105 110
 Gly Asp Pro Thr Cys Cys Phe Val Leu Asp Leu Val Cys Thr Trp Phe
 115 120 125
 Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly
 130 135 140
 Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys Lys
 145 150 155 160
 Ile Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu
 165 170 175
 Met Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Cys Tyr
 180 185 190
 Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly
 195 200 205
 Asn Ile Asn Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu
 210 215 220
 Lys Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Asn Leu Leu
 225 230 235 240
 Leu Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe
 245 250 255
 Val Phe Phe Ile Phe Gly Ile Ile Gly Val Gln Leu Trp Ala Gly Leu
 260 265 270
 Leu Arg Asn Arg Cys Phe Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp
 275 280 285
 Val Ala Leu Pro Pro Tyr Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro
 290 295 300

a
6
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 Ile Pro Pro Leu Lys Glu Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp
 325 330 335
 Asp Val Tyr Asp Phe Gly Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly
 340 345 350
 Leu Cys Val Asn Trp Asn Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser
 355 360 365
 Ala Asn Pro His Lys Gly Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala
 370 375 380
 Trp Ile Val Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Glu Ile
 385 390 395 400
 Met Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe
 405 410 415
 Ile Leu Leu Ile Ile Ser Glu Leu Ile His Leu Val Met Pro Asp Cys
 420 425 430
 Ser Phe Ser Thr Ala Gln Ser Pro Lys Cys Gln Gly Asp Ser Leu Pro
 435 440 445
 Gly Val Ala Ala Glu Ser Leu Leu Leu Arg Asp Ser Ser Ser Ser Val
 450 455 460
 Ile Thr Asp Glu Ala Ala Met Glu Asn Leu Leu Ala Gly Thr Ser
 465 470 475 480
 Lys Gly Asp Glu Ser Tyr Leu Leu Arg Leu Ala Gly Ser Gln Val His
 485 490 495
 Ser Gln Ala Gln Gln Met Leu Gly Arg Gly Leu Gly Pro Glu Ser Leu
 500 505 510
 Glu Thr Gly Glu Glu Pro His Ser Trp Ser Pro Arg Ala Thr Arg Arg
 515 520 525
 Trp Asp Pro Gln Cys Gln Pro Gly Gln Pro Leu Pro Leu His Phe Met
 530 535 540
 Gln Ala Gln Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val
 545 550 555 560
 Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu His Arg Leu Met
 565 570 575
 Leu Glu Gln Arg Gln Arg Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr
 580 585 590
 Ala Glu Pro Gly Asp Cys Tyr Glu Glu Ile Phe Gln Tyr Val Cys His
 595 600 605
 Ile Leu Arg Lys Ala Lys Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu
 610 615 620
 Gln Ser Arg Arg Gln Ala Leu Gly Pro Glu Ala Pro Ala Pro Ala Lys
 625 630 635 640
 Pro Gly Pro His Ala Lys Glu Pro Arg His Tyr Pro Leu Thr Val Trp
 645 650 655
 Glu Ser Ile Leu Gly Arg Gln Ala Glu Glu Cys Thr Leu Arg Ala Ala
 660 665 670
 Ala His Pro Ser Ser Gly Ala Ser His Pro Gly Val Gly Ser Glu Glu
 675 680 685
 Ala Pro Glu Leu Cys Pro Gln His Ser Pro Leu Asp Ala Thr Pro His
 690 695 700
 Thr Leu Val Gln Pro Ile Pro Ala Thr Leu Ala Ser Asp Pro Ala Ser
 705 710 715 720
 Cys Pro Cys Cys Gln His Glu Asp Gly Arg Arg Pro Ser Gly Leu Gly
 725 730 735
 Ser Thr Asp Ser Gly Gln Glu Gly Ser Gly Ser Gly Ser Ser Ala Gly
 740 745 750
 Gly Glu Asp Glu Ala Asp Gly Asp Gly Ala Arg Ser Ser Glu Asp Gly

a6
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770	775	780
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785	790	795
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805	810	815
Ala Ile Leu Val Asn Thr Val Ser Met Gly Ile Glu His His Glu Gln		
820	825	830
Ala Ser Ala Ala Gln Pro Gly Arg Ala Cys Gly Arg Gly Gln Asn Pro		
835	840	845
Asp Leu Cys Met Thr Leu Lys Ala Pro Cys Leu Cys His Asn Val Pro		
850	855	860
Ser Pro Gly Gln Gly Val Leu Ser His Pro Val Thr Pro Pro His Thr		
865	870	875
Ala Pro Trp Arg Met Glu Thr Gly Lys Gln Gly His Gly Cys Glu Glu		
885	890	895
Gly Pro Gly Gln Arg Ser Ser Asp Met Phe Ala Leu Glu Met Ile Leu		
900	905	910
Lys Leu Ala Ala Phe Gly Leu Phe Asp Tyr Leu Arg Asn Pro Tyr Asn		
915	920	925
Ile Phe Asp Ser Ile Ile Val Ile Ile Ser Ile Trp Glu Ile Val Gly		
930	935	940
Gln Ala Asp Gly Gly Leu Ser Val Leu Arg Thr Phe Arg Leu Leu Arg		
945	950	955
Val Leu Lys Leu Val Arg Phe Met Pro Ala Leu Arg Arg Gln Leu Val		
965	970	975
Val Leu Met Lys Thr Met Asp Asn Val Ala Thr Phe Cys Met Leu Leu		
980	985	990
Met Leu Phe Ile Phe Ile Phe Ser Ile Leu Gly Met His Ile Phe Gly		
995	1000	1005
Cys Lys Phe Ser Leu Arg Thr Asp Thr Gly Asp Thr Val Pro Asp Arg		
1010	1015	1020
Lys Asn Phe Asp Ser Leu Leu Trp Ala Ile Val Thr Val Phe Gln Ile		
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Leu Thr Gln Glu Asp Trp Asn Val Val Leu Tyr Asn Gly Met Ala Ser		
1045	1050	1055
Thr Ser Pro Trp Ala Ser Leu Tyr Phe Val Ala Leu Met Thr Phe Gly		
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Asn Tyr Val Leu Phe Asn Leu Leu Val Ala Ile Leu Val Glu Gly Phe		
1075	1080	1085
Gln Ala Glu Val Thr Val Val Leu Ala Glu Glu Ala Pro Pro Gln Gly		
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Leu Arg Lys Thr Gly Arg Gly Arg Gly Leu Asp Gly Gly Leu		
1105	1110	1115
Gln Phe Lys Leu Leu Ala Gly Asn Leu Ser Leu Lys Glu Gly Val Ala		
1125	1130	1135
Asp Glu Val Gly Asp Ala Asn Arg Ser Tyr Ser Asp Glu Asp Gln Ser		
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Leu Asp Pro Ser Leu Pro Leu Gly Gly His Leu Gly Pro Ala Gly Ala		
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Ala Gly Pro Ala Pro Arg Leu Ser Leu Gln Pro Asp Pro Met Leu Val		
1205	1210	1215

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1235 1240 1245
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Gly Ala Asp Pro Asn Gly Asn Ser Phe Gln Ser Ser Ser Arg Ser Ser
1265 1270 1275 1280
Tyr Tyr Gly Pro Trp Gly Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser
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Ser Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu His Glu Ser
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Gly Pro Ala Pro Gly His Glu Asp Cys Asn Gly Arg Met Pro Ser Ile
1395 1400 1405
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Lys Val Gly Asp Leu Val Val Trp Val Tyr Gly Gln Arg Arg Gln Arg
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Ala Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn Tyr Ile Phe
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Thr Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser Leu Gly
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1570 1575 1580
Asp Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val Val Ser Leu
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Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Val Leu Arg
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1620 1625 1630
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1635 1640 1645
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1650 1655 1660
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1715	1720		1725
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Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ser			
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Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His			
1765	1770		1775
Lys Cys Arg Gln His Gln Glu Ala Glu Glu Ala Arg Arg Arg Glu Glu			
1780	1785		1790
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Arg Leu			
1795	1800		1805
Pro Tyr Tyr Ala Thr Tyr Cys His Thr Arg Leu Leu Ile His Ser Met			
1810	1815		1820
Cys Thr Ser His Tyr Leu Asp Ile Phe Ile Thr Phe Ile Ile Cys Leu			
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<210> 19
<211> 567
<212> DNA
<213> *Homo sapiens*

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<212> PRT
<213> *Homo sapiens*

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   20          25          30
Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu
   35          40          45
Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
   50          55          60
Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser Gly Asp

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Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr			
115	120	125	
Tyr Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly Ala Ile			
130	135	140	
Ser Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln Val Ile			
145	150	155	160
Thr Leu Glu Gly Trp Val Ala Ile Met Tyr Tyr Val Met Asp Ala Leu			
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 <212> DNA
 <213> Rattus

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 <213> Rattus

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 35 40 45
 Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
 50 55 60
 Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Thr Gly Asp
 65 70 75 80
 Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly
 85 90 95
 Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly
 100 105 110
 Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr
 115 120 125
 Tyr Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile

Ab
 Conf

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Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp Ala His		160
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Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile		
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<213> Rattus

<400> 23

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a6
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 Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
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a6
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ab
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Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe	Ile Tyr Phe Ile	
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Ser Ala Leu Glu Asp Pro Glu Phe Glu Phe Ser	Gly Ser Glu Ser Gly	
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A
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275	280	285
Arg Glu Val Cys Leu Ser Lys	Asp Asp Val Tyr Asp Phe	Gly Ala Gly
290	295	300
Arg Gln Asp Leu Asn Ala Ser	Gly Leu Cys Val Asn Trp Asn	Arg Tyr
305	310	315
Tyr Asn Val Cys Arg Thr Gly	Asn Ala Asn Pro His Lys	Gly Ala Ile
325	330	335
Asn Phe Asp Asn Ile Gly Tyr	Ala Trp Ile Val Ile Phe Gln	Val Ile
340	345	350
Thr Leu Glu Gly Trp Val Glu	Ile Met Tyr Tyr Val Met	Asp Ala His
355	360	365
Ser Phe Tyr Asn Phe Ile Leu	Ile Ile Val Gly Ser Phe Phe Met	
370	375	380
Ile Asn Leu Cys Leu Val Leu	Ile Ala Thr Gln Phe Ser Glu	Thr Lys
385	390	395
Gln Arg Asn His Arg Leu Met	Leu Glu Gln Arg Gln Arg	Tyr Leu Ser
405	410	415
Ser Ser Thr Val Ala Ser Tyr	Ala Glu Pro Gly Asp Cys	Tyr Glu Glu
420	425	430
Ile Phe Gln Tyr Val Cys His	Ile Leu Arg Lys Ala Lys	Arg Arg Ala
435	440	445
Leu Gly Leu Tyr Gln Ala Leu	Gln Asn Arg Arg Gln Ala Met	Gly Pro
450	455	460
Gly Thr Pro Ala Pro Ala Lys	Pro Gly Pro His Ala Lys	Glu Pro Ser
465	470	475
His Ser Lys Leu Cys Pro Arg	His Ser Pro Leu Asp Pro	Thr Pro His
485	490	495
Thr Leu Val Gln Pro Ile Ser	Ala Ile Leu Ala Ser Tyr	Pro Ser Ser
500	505	510
Cys Pro His Cys Gln His Glu	Ala Gly Arg Arg Pro Ser	Gly Leu Gly
515	520	525
Ser Thr Asp Ser Gly Gln Glu	Gly Ser Gly Gly Ser Ala	Glu
530	535	540
Ala Glu Ala Asn Gly Asp	Gly Leu Gln Ser Arg Glu	Asp Gly Val Ser
545	550	555
Ser Asp Leu Gly Lys Glu	Glu Gln Glu Asp Gly Ala	Ala Arg Leu
565	570	575
Cys Gly Asp Val Trp Arg Glu	Thr Arg Lys Lys Leu Arg	Gly Ile Val
580	585	590
Asp Ser Lys Tyr Phe Asn Arg	Gly Ile Met Met Ala Ile	Leu Val Asn
595	600	605
Thr Val Ser Met Gly Ile Glu	His His Glu Gln Pro	Glu Glu Leu Thr
610	615	620
Asn Ile Leu Glu Ile Cys Asn	Val Val Phe Thr Ser Met	Phe Ala Leu
625	630	635
		640

ab
cont

Glu Met Ile Leu Lys Leu Ala Ala Phe Gly Leu Phe Asp Tyr Leu Arg
 645 650 655
 Asn Pro Tyr Asn Ile Phe Asp Ser Ile Ile Val Ile Ile Ser Ile Trp
 660 665 670
 Glu Ile Val Gly Gln Ala Asp Ser Gly Leu Ser Val Leu Arg Thr Ser
 675 680 685
 Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe Met Pro Ala Leu Arg
 690 695 700
 Gln Leu Val Val Leu Met Lys Thr Met Asp Asn Val Ala Thr Phe Cys
 705 710 715 720
 Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser Ile Leu Gly Ile Asp
 725 730 735
 Ile Phe Gly Cys Lys Phe Ser Leu Arg Thr Asp Thr Gly Asp Thr Val
 740 745 750
 Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala Ile Val Thr Val
 755 760 765
 Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Val Val Leu Tyr Asn Gly
 770 775 780
 Met Ala Ser Thr Thr Pro Trp Ala Ser Leu Tyr Phe Val Ala Leu Met
 785 790 795 800
 Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val Ala Ile Leu Val
 805 810 815
 Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Arg Ser Tyr Ser Asp Glu
 820 825 830
 Asp Gln Ser Ser Ser Asn Leu Glu Glu Leu Asp Lys Leu Pro Glu Gly
 835 840 845
 Leu Asp Asn Arg Arg Asp Leu Lys Leu Cys Pro Ile Pro Met Thr Pro
 850 855 860
 Asn Gly His Leu Asp Pro Ser Leu Pro Leu Gly Ala His Leu Gly Pro
 865 870 875 880
 Ala Gly Thr Met Gly Thr Ala Pro Arg Leu Ser Leu Gln Pro Asp Pro
 885 890 895
 Val Leu Val Ala Arg Asp Ser Arg Lys Ser Ser Tyr Trp Ser Leu Gly
 900 905 910
 Arg Met Ser Tyr Asp Gln Arg Ser Leu Ser Ser Ser Arg Ser Ser Tyr
 915 920 925
 Tyr Gly Pro Gly Gly Arg Ser Gly Thr Trp Ala Ser Arg Arg Ser Ser
 930 935 940
 Trp Asn Ser Leu Lys His Lys Pro Pro Ser Ala Glu His Glu Ser Leu
 945 950 955 960
 Leu Ser Gly Glu Gly Gly Ser Cys Val Arg Ala Cys Glu Gly Ala
 965 970 975
 Arg Glu Glu Ala Pro Thr Arg Thr Ala Pro Leu His Ala Pro His Arg
 980 985 990
 His His Ala His His Gly Pro His Leu Ala His Arg His Arg His His
 995 1000 1005
 Arg Arg Thr Leu Ser Leu Asp Thr Arg Asp Ser Val Asp Leu Gly Glu
 1010 1015 1020
 Leu Val Pro Val Val Gly Ala His Ser Arg Ala Ala Trp Arg Gly Ala
 1025 1030 1035 1040
 Gly Gln Ala Pro Gly His Glu Asp Cys Asn Gly Arg Met Pro Asn Met
 1045 1050 1055
 Ala Lys Asp Val Phe Thr Lys Met Asp Asp Arg Arg Asp Arg Gly Glu
 1060 1065 1070
 Asp Glu Glu Glu Ile Asp Tyr Thr Leu Cys Phe Arg Val Arg Lys Met
 1075 1080 1085
 Ile Cys Cys Val Tyr Lys Pro Asp Trp Cys Glu Val Arg Glu Asp Trp

ab
 cont

1090 1095 1100
 Ser Val Tyr Leu Phe Ser Pro Glu Asn Lys Phe Arg Ile Leu Cys Gln
 1105 1110 1115 1120
 Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val Leu Ala Phe Ile
 1125 1130 1135
 Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro Gln Ile Glu Ala
 1140 1145 1150
 Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn Tyr Ile Phe Thr
 1155 1160 1165
 Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val Ser Leu Gly Leu
 1170 1175 1180
 Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Thr Asp Trp Asn Val Leu Asp
 1185 1190 1195 1200
 Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val Val Ser Val Ala
 1205 1210 1215
 Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg Leu Leu Arg Thr
 1220 1225 1230
 Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Pro Gly Leu Lys Leu Val
 1235 1240 1245
 Val Glu Thr Leu Ile Ser Ser Leu Lys Pro Ile Gly Asn Ile Val Leu
 1250 1255 1260
 Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val Gln Leu
 1265 1270 1275 1280
 Phe Lys Gly Lys Phe Tyr His Cys Leu Gly Val Asp Thr Arg Asn Ile
 1285 1290 1295
 Thr Asn Arg Ser Asp Cys Val Ala Ala Asn Tyr Arg Trp Val His His
 1300 1305 1310
 Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu Phe Val
 1315 1320 1325
 Leu Ala Ser Lys Asp Gly Trp Val Asn Ile Met Tyr Asn Gly Leu Asp
 1330 1335 1340
 Ala Val Ala Val Asp Gln Gln Pro Val Thr Asn His Asn Pro Trp Met
 1345 1350 1355 1360
 Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ser Phe Phe Val Leu
 1365 1370 1375
 Asn Met Phe Val Gly Val Val Glu Asn Phe His Lys Cys Arg Gln
 1380 1385 1390
 His Gln Glu Ala Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg
 1395 1400 1405
 Arg Leu Glu Lys Lys Arg Arg Tyr Ala Gln Arg Leu Pro Tyr Tyr Ala
 1410 1415 1420
 Thr Tyr Cys Pro Thr Arg Leu Leu Ile His Ser Met Cys Thr Ser His
 1425 1430 1435 1440
 Tyr Leu Asp Ile Phe Ile Thr Phe Ile Ile Cys Leu Asn Val Val Thr
 1445 1450 1455
 Met Ser Leu Glu His Tyr Asn Gln Pro Thr Ser Leu Glu Thr Ala Leu
 1460 1465 1470
 Lys Tyr Cys Asn Tyr Met Phe Thr Thr Val Phe Val Leu Glu Ala Val
 1475 1480 1485
 Leu Lys Leu Val Ala Phe Gly Leu Arg Arg Phe Phe Lys Asp Arg Trp
 1490 1495 1500
 Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Val Met Gly Ile Thr
 1505 1510 1515 1520
 Leu Glu Glu Ile Glu Ile Asn Ala Ala Leu Pro Ile Asn Pro Thr Ile
 1525 1530 1535
 Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu
 1540 1545 1550

ab
 cont

Lys Met Ala Thr Gly Met Arg Ala Leu Leu Asp Thr Val Val Gln Ala
 1555 1560 1565
 Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe
 1570 1575 1580
 Ile Tyr Ala Ala Leu Gly Val Glu Leu Phe Gly Lys Leu Val Cys Asn
 1585 1590 1595 1600
 Asp Glu Asn Pro Cys Glu Gly Met Ser Arg His Ala Thr Phe Glu Asn
 1605 1610 1615
 Ser Ala Arg Ala Phe Leu Thr Leu Phe Gln Val Ser Thr Gly Asp Asn
 1620 1625 1630
 Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys Thr His Asp Glu
 1635 1640 1645
 Arg Thr Cys Leu Ser Ser Leu Gln Phe Val Ser Pro Leu Tyr Phe Val
 1650 1655 1660
 Ser Phe Val Leu Thr Ala Gln Phe Val Leu Ile Asn Val Val Val Ala
 1665 1670 1675 1680
 Val Leu Met Lys His Leu Asp Asp Ser Asn Lys Glu Ala Gln Glu Asp
 1685 1690 1695
 Ala Glu Met Asp Ala Glu Ile Glu Leu Glu Met Ala His Gly Ser Gly
 1700 1705 1710
 Pro Cys Pro Gly Pro Cys Pro Gly Pro Cys Pro Cys Pro Cys Pro Cys
 1715 1720 1725
 Pro Cys Ser Gly Pro Arg Cys Pro Leu Val Thr Trp Gly Ser Gly Ala
 1730 1735 1740
 Met Asp Arg Glu Gly Gln Val Leu Glu Ala His Arg Glu Ser Pro Val
 1745 1750 1755 1760
 Arg Thr Ala Ile Arg Cys Trp Thr Pro Arg Val Thr Cys Ala Gly Thr
 1765 1770 1775
 Ala Ile Leu Gln Pro Arg Arg Pro Cys Gly Trp Thr Gly Ser Leu Glx
 1780 1785 1790

ab
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 <210> 29
 <211> 540
 <212> DNA
 <213> Rattus

<400> 29
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 ccgaaaagca gcccgaaggc tggcccaggt ctctagggtc ataggcggtc gggctggct 120
 gctcagcagc ccagtggccc gtagtggca ggagccccag cccagtggca gctgcactcg 180
 ctcacaccgt cgctctgtctg tccaccaccc ggtccaccac catcaccacc accatcacca 240
 ctaccacctg ggtaatggga cgctcagagt tccccgggccc agcccagaga tccaggacag 300
 ggatgccaat gggctcgcc ggctcatgct accaccaccc tctacaccca ctcccctctgg 360
 gggccctccg aggggtgcgg agtctgtaca cagttctac catgctgact gccacttgaa 420
 gccagtcgt tgccaggcac cccctccag atgcccacatcg gaggcatctg gttaggactgt 480
 gggtagtggg aaggtgttacc ccactgtgca taccagccct ccaccagaga tactgaaggaa 540

<210> 30
 <211> 2212
 <212> DNA
 <213> Homo sapiens

<400> 30
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 gcgccggcggc gggttccct gcgccccggc gccccgggg cagcatcccc ctgcggggcag 120

ggggagctgg gctgaactgg ccctcccgaa ggctcagctt gcgcctaga gccaccaga 180
 tgtcccccg ccggggccccg cgggttgcgt gaggacacct cctctgagggg gcgcgcctg 240
 cccctctccg gatcgcccg ggcggccgt ggccagagga tggacgagga ggaggatgga 300
 gcgggcgcg aggagtccgg acagcccg agttcatgc ggctcaacga cctgtcgaaa 360
 gcccggggcc ggcggggcc ggggtcagca gaaaaggacc cggcagcgc ggactccgag 420
 gcggaggggc tgccgtaccc ggcgtggcc cgggtggttt tcttcactt gagccaggac 480
 agccgcccgc ggagctggg tctccgcacg gctctgtaacc cctgggttga ggcgcacgc 540
 atgttggtca tccttctcaa ctgcgtgacc ctgggcatgt tccggccatg cgaggacatc 600
 gcctgtgact cccagcgtg cggatccctg caggcctttt atgacttcat ctttgccctc 660
 tttccgtgg agatgggtt gaagatggg gccttggca tctttggaa aaagtgttac 720
 ctgggagaca cttggAACCG gcttgactt ttcatcgta tcgcaggat gctggagtac 780
 tcgctggacc tgcaaacgt cagttctca gctgtcagga cagtcgtgt gctgcgacccg 840
 ctcaggggcca ttaaccgggt gcccagcatg cgcatttc tcacgttgc gctggatacg 900
 ctgcccattgc tggcaacgt cctgctgctc tgcttcttc tcttcttcat cttcgccatc 960
 gtcggcgcc agctgtggc agggctgtt cggAACCGAT gcttcctacc tgagaatttc 1020
 agcctcccccc tgacgtggaa cctggagcgc tattaccaga cagagaacga ggtgagagc 1080
 cccttcattct gctcccagcc acgcgagaac ggcattgcggt cctgcagaag cgtgcccacg 1140
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 tccagcaaca ccacctgtgt caactggAACAC cagttactaca ccaactgctc agcggggggag 1260
 cacaacccct tcaaggggcgc catcaactt gacaacattt gctatgcctg gatcgccatc 1320
 ttccagggtca tcacgtggaa gggctgggtc gacatcatgt actttgtat ggtgctcat 1380
 tccttctaca atttcattcta cttcatcctc cttcatcatcg tggccatc tttcatgatc 1440
 aacctgtgcc tgggtgtat tgccacgcg ttctcagaga ccaaggcgcg gaaaagccag 1500
 ctgatgcggg agcagcgtgt ggggttctg tccaaacgcgc gcaccttggc tagttctt 1560
 gagccggca gctgttatga ggagctgctc aagtacctgg tgtacatcct tcgtaaggca 1620
 gcccgcaggc tggctcagggt ctctcggca gcagggtgtgc ggggtgggt gctcgcgc 1680
 ccagcaccct tcggggggca ggagacccag cccagcgcgc gctgtctcg ctccccaccgc 1740
 cgcctatccg tccaccaccc ggtgcaccac caccaccacc atcaccacca ctaccacctg 1800
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 gggcccggcc ggtcattgtct gccaccaccc tcgacgcctg ccctcccg gggccccccct 1920
 ggtggcgcag agtctgtgc cagttctac catgcgcact gcaactttaga gcaacttgc 1980
 tgccaggcgc cccctccctt gtccttcatc tggcatccg gcaggactgt gggcaggcggg 2040
 aagggttatac ccaccgtgc caccagccct ccaccggaga cgctgaagga gaaggcacta 2100
 gtagaggtgg ctgcccagctc tggcccccacccttccca gcctcaacat cccacccggg 2160
 ccctacagct ccatgcacaa gctgtggag acacagagta caggtgcctg cc 2212

a⁶
cont

<210> 31
 <211> 644
 <212> PRT
 <213> Homo sapiens

<400> 31
 Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
 1 5 10 15
 Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
 20 25 30
 Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
 35 40 45
 Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
 50 55 60
 Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
 65 70 75 80
 Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
 85 90 95
 Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
 100 105 110
 Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe

115 120 125
 Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
 130 135 140
 Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
 145 150 155 160
 Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
 165 170 175
 Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
 180 185 190
 Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Asp Thr Leu
 195 200 205
 Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
 210 215 220
 Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
 225 230 235 240
 Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
 245 250 255
 Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
 260 265 270
 Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
 275 280 285
 Arg Gly Asp Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
 290 295 300
 Tyr Asn Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
 305 310 315 320
 Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
 325 330 335
 Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
 340 345 350
 Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
 355 360 365
 Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Val Gly Ser Phe
 370 375 380
 Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
 385 390 395 400
 Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
 405 410 415
 Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
 420 425 430
 Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
 435 440 445
 Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
 450 455 460
 Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
 465 470 475 480
 Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
 485 490 495
 His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
 500 505 510
 Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
 515 520 525
 Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
 530 535 540
 Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
 545 550 555 560
 Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
 565 570 575

ab
 cont

Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
580 585 590
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
595 600 605
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
610 615 620
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625 630 635 640
Thr Gly Ala Cys

<210> 32
<211> 1608
<212> DNA
<213> Homo sapiens

<400> 32
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aggcgcacg ggccgcggac gaggtccggg tgccccctggg cgcgcggccccc cctggccctg 120
cgcgcttgggt gggggcggtcc cggagagcc ccggggcgcc gggacgcgag gcggagcgccc 180
ggtccgagct cggcggtgtca ccctccggaga gcccggcgcc cgagcgcggc gcggagctgg 240
gtgccgcacga ggagcagcgc gtcccggtacc cggccttggc ggcacggtc ttcttctgcc 300
tcggtcagac cacgcggcccg cgcagctggt gcctccggct ggtctcaac ccatggttcg 360
agcacgttagt catgtcggtta atcatgtca actgcgtgac cctgggcattt ttccggccct 420
gtgaggacgt ttagtgcggc tccgagcgct gcaacatccct ggaggccctt gacgccttca 480
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agaagtgtta cctgggtgac acgtggaaaca ggctggattt cttcatcgac gtggcgggca 600
tgatggagta ctcgttggac ggacacaacg tgagcctctc ggctatcagg accgtgcggg 660
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agggcgagga gaacccgttc atctgtcctt cacgcccggaa caacggcatg cagaagtgt 960
cgcacatccc cggccgcgcg gagctgcgc tggccctgcac cctggctgg gaggcctaca 1020
cgcaaggcca ggcccggggg gtggcgctg cacgcacgc ctgcataac ttggaaaccgt 1080
actacaacgt gtgcgcctcg ggtgactcca accccccacaa cgggtccatc aacttcgaca 1140
acatcggtcta cgcctggatc gccatcttc aggtgatcac gctggaaaggc tgggtggaca 1200
tcatgtacta cgtcatggac gcccactcat tctacaactt catctattt atcctgtca 1260
tcatcggtgg ctccttcttc atgatcaacc tgcgcctggg ggtgattgcc acgcagttt 1320
cgagacgaa gcagcggggag agtcagctga tgcgggagca gcgggcacgc cacctgtcca 1380
acgacagcac gctggccagc ttctccggac ctggcagctg ctacgaagag ctgctgaagt 1440
acgtggggcca catattccgc aaggtcaagc ggcgcagctt ggcctctac gcccgtggc 1500
agagccgctg ggcgaagaag gtggacccca gtgtgtgca aggccagggt cccgggcacc 1560
gccagcgcgg ggcaggcagg cacacagcct cggcgcacca cctggct 1608

<210> 33
<211> 518
<212> PRT
<213> Homo sapiens

<400> 33
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1 5 10 15
Ala Pro Pro Pro Gly Pro Ala Ala Leu Val Gly Ala Ser Pro Glu Ser
20 25 30
Pro Gly Ala Pro Gly Arg Glu Ala Glu Arg Gly Ser Glu Leu Gly Val

35	40	45
Ser Pro Ser Glu Ser Pro Ala Ala Glu Arg Gly Ala Glu Leu Gly Ala		
50	55	60
Asp Glu Glu Gln Arg Val Pro Tyr Pro Ala Leu Ala Ala Thr Val Phe		
65	70	75
Phe Cys Leu Gly Gln Thr Thr Arg Pro Arg Ser Trp Cys Leu Arg Leu		
85	90	95
Val Cys Asn Pro Trp Phe Glu His Val Ser Met Leu Val Ile Met Leu		
100	105	110
Asn Cys Val Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Val Glu Cys		
115	120	125
Gly Ser Glu Arg Cys Asn Ile Leu Glu Ala Phe Asp Ala Phe Ile Phe		
130	135	140
Ala Phe Phe Ala Val Glu Met Val Ile Lys Met Val Ala Leu Gly Leu		
145	150	155
Phe Gly Gln Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe		
165	170	175
Phe Ile Val Val Ala Gly Met Met Glu Tyr Ser Leu Asp Gly His Asn		
180	185	190
Val Ser Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Arg		
195	200	205
Ala Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu		
210	215	220
Asp Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val		
225	230	235
Phe Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu		
245	250	255
Arg Asn Arg Cys Phe Leu Asp Ser Ala Phe Val Arg Asn Asn Asn Leu		
260	265	270
Thr Phe Leu Arg Pro Tyr Tyr Gln Thr Glu Glu Gly Glu Glu Asn Pro		
275	280	285
Phe Ile Cys Ser Ser Arg Arg Asp Asn Gly Met Gln Lys Cys Ser His		
290	295	300
Ile Pro Gly Arg Arg Glu Leu Arg Met Pro Cys Thr Leu Gly Trp Glu		
305	310	315
Ala Tyr Thr Gln Pro Gln Ala Glu Gly Val Gly Ala Ala Arg Asn Ala		
325	330	335
Cys Ile Asn Trp Asn Gln Tyr Tyr Asn Val Cys Arg Ser Gly Asp Ser		
340	345	350
Asn Pro His Asn Gly Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala Trp		
355	360	365
Ile Ala Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met		
370	375	380
Tyr Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile		
385	390	395
Leu Leu Ile Ile Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val		
405	410	415
Val Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu		
420	425	430
Met Arg Glu Gln Arg Ala Arg His Leu Ser Asn Asp Ser Thr Leu Ala		
435	440	445
Ser Phe Ser Glu Pro Gly Ser Cys Tyr Glu Glu Leu Leu Lys Tyr Val		
450	455	460
Gly His Ile Phe Arg Lys Val Lys Arg Arg Ser Leu Arg Leu Tyr Ala		
465	470	475
Arg Trp Gln Ser Arg Trp Arg Lys Lys Val Asp Pro Ser Ala Val Gln		
485	490	495

a
cont

Gly Gln Gly Pro Gly His Arg Gln Arg Arg Ala Gly Arg His Thr Ala
500 505 510
Ser Val His His Leu Val
515

<210> 34
<211> 1080
<212> DNA
<213> Homo sapiens

<400> 34
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acagcctcaa gcacaagccg ccgtcggccg agcatgagtc cctgctctc gcggagcgcg 180
gcggcggcgc cccggtctgc gaggttgcgg cggacgaggg gcccgcgcg gccgcacccc 240
tgcacacccc acacgccccac cacattcatc acgggccccca tctggcgcac cggccaccggc 300
accaccggcg gacgctgtcc ctcgacaaca gggactcggt ggacctggcc gagctggtgc 360
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Ala Glu His Glu Ser Leu Leu Ser Ala Glu Arg Gly Gly Gly Ala Arg
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Val Cys Glu Val Ala Ala Asp Glu Gly Pro Pro Arg Ala Ala Pro Leu
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His Thr Pro His Ala His His Ile His His Gly Pro His Leu Ala His
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Arg His Arg His His Arg Arg Thr Leu Ser Leu Asp Asn Arg Asp Ser
100 105 110
Val Asp Leu Ala Glu Leu Val Pro Ala Val Gly Ala His Pro Arg Ala
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Ala Trp Arg Ala Ala Gly Pro Ala Pro Gly His Glu Asp Cys Asn Gly
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Arg Met Pro Ser Ile Ala Lys Asp Val Phe Thr Lys Met Gly Asp Arg

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Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro Asp Trp Cys Glu Val			
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Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro Glu Asn Arg Phe Arg			
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Val Leu Cys Gln Thr Ile Ile Ala His Lys Leu Phe Asp Tyr Val Val			
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Leu Ala Phe Ile Phe Leu Asn Cys Ile Thr Ile Ala Leu Glu Arg Pro			
225	230	235	240
Gln Ile Glu Ala Gly Ser Thr Glu Arg Ile Phe Leu Thr Val Ser Asn			
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Tyr Ile Phe Thr Ala Ile Phe Val Gly Glu Met Thr Leu Lys Val Val			
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Ser Leu Gly Leu Tyr Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp			
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Asn Val Leu Asp Gly Phe Leu Val Phe Val Ser Ile Ile Asp Ile Val			
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Val Ser Leu Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly Val Leu Arg			
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Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg			
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Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
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a
b
cnt

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a
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 1490 1495 1500
 Pro Ile Met Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe
 1505 1510 1515 1520
 Leu Leu Ile Val Ala Phe Phe Val Leu Asn Met Phe Val Gly Val Val
 1525 1530 1535
 Val Glu Asn Phe His Lys Cys Arg Gln His Gln Glu Glu Glu Ala
 1540 1545 1550
 Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg
 1555 1560 1565
 Lys Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu
 1570 1575 1580
 Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr
 1585 1590 1595 1600
 Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His Tyr Gln
 1605 1610 1615
 Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe
 1620 1625 1630
 Thr Val Ile Phe Val Leu Glu Ser Val Phe Lys Leu Val Ala Phe Gly
 1635 1640 1645
 Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile
 1650 1655 1660
 Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn
 1665 1670 1675 1680
 Ala Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu
 1685 1690 1695
 Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg
 1700 1705 1710
 Ala Leu Leu Asp Thr Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu
 1715 1720 1725
 Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val
 1730 1735 1740
 Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly
 1745 1750 1755 1760
 Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr
 1765 1770 1775
 Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp
 1780 1785 1790
 Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile
 1795 1800 1805
 Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu
 1810 1815 1820
 Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu Ser Asn
 1825 1830 1835 1840
 Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu
 1845 1850 1855
 Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe
 1860 1865 1870
 Leu Trp Pro Gly Val Glu Gly Pro Asp Ser Pro Asp Ser Pro Lys Pro
 1875 1880 1885
 Gly Ala Leu His Pro Ala Ala His Ala Arg Ser Ala Ser His Phe Ser
 1890 1895 1900
 Leu Glu His Pro Thr Met Gln Pro His Pro Thr Glu Leu Pro Gly Pro
 1905 1910 1915 1920

a
Cont

Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu
 1925 1930 1935
 Pro Asn Asp Ser Tyr Met Cys Arg His Gly Ser Thr Ala Glu Gly Pro
 1940 1945 1950
 Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Val
 1955 1960 1965
 Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Tyr Ile Leu Gln Leu
 1970 1975 1980
 Pro Lys Asp Ala Pro His Leu Leu Gln Pro His Ser Ala Pro Thr Trp
 1985 1990 1995 2000
 Gly Thr Ile Pro Lys Leu Pro Pro Gly Arg Ser Pro Leu Ala Gln
 2005 2010 2015
 Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val
 2020 2025 2030
 Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ala Glu Val Ser Gly Pro
 2035 2040 2045
 Ser Pro Pro Leu Ala Arg Ala Tyr Ser Phe Trp Gly Gln Ser Ser Thr
 2050 2055 2060
 Gln Ala Gln Gln His Ser Arg Ser His Ser Lys Ile Ser Lys His Met
 2065 2070 2075 2080
 Thr Pro Pro Ala Pro Cys Pro Gly Pro Glu Pro Asn Trp Gly Lys Gly
 2085 2090 2095
 Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp
 2100 2105 2110
 Ile Ser Gly Asp Leu Leu Pro Pro Gly Gly Gln Glu Pro Pro Ser
 2115 2120 2125
 Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Ala Gln Ser Cys Gln
 2130 2135 2140
 Arg Arg Pro Thr Ser Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala
 2145 2150 2155 2160
 Val Ser Cys Leu Asp Ser Gly Ser Gln Pro His Leu Gly Thr Asp Pro
 2165 2170 2175
 Ser Asn Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys
 2180 2185 2190
 Lys Lys Leu Ser Pro Pro Ser Ile Thr Ile Asp Pro Pro Glu Ser Gln
 2195 2200 2205
 Gly Pro Arg Thr Pro Pro Ser Pro Gly Ile Cys Leu Arg Arg Arg Ala
 2210 2215 2220
 Pro Ser Ser Asp Ser Lys Asp Pro Leu Ala Ser Gly Pro Pro Asp Ser
 2225 2230 2235 2240
 Met Ala Ala Ser Pro Ser Pro Lys Lys Asp Val Leu Ser Leu Ser Gly
 2245 2250 2255
 Leu Ser Ser Asp Pro Ala Asp Leu Asp Pro
 2260 2265

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 <213> C. elegans

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 Glu Gly Trp Thr Asp Phe Glu Thr Leu Ser Phe Lys Gly Trp Asn Val
 20 25 30
 Ile Arg Cys Leu Thr Gly Glu Asp Trp Asn Asp Ile

<210> 39
<211> 44
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<213> C. elegans

<400> 39
Leu Ala Ala Ser Gln Glu Gly Trp Val Tyr Val Gln Ile Ile Thr Gln
1 5 10 15
Glu Gly Trp Thr Asp Val Glu Thr Leu Ser Tyr Lys Gly Trp Asn Val
20 25 30
Val Arg Ser Val Thr Gly Glu Asp Trp Asn Asp Ile
35 40

<210> 40
<211> 44
<212> PRT
<213> Rattus

<400> 40
Glu Ala Ser Ser Gln Glu Gly Trp Val Phe Leu Gln Ile Leu Thr Gln
1 5 10 15
Glu Gly Trp Val Asp Val Glu Val Leu Ser Leu Lys Gly Trp Val Glu
20 25 30
Val Arg Ile Val Thr Gly Glu Asp Trp Asn Lys Ile
35 40

a^b
ant
<210> 41
<211> 44
<212> PRT
<213> Unknown

<220>
<223> Mammalian L-Type Ca Channel

<400> 41
Gln Cys Ile Thr Met Glu Gly Trp Thr Asp Val Gln Ile Leu Thr Gly
1 5 10 15
Glu Asp Trp Asn Ser Val Thr Val Ser Thr Phe Glu Gly Trp Pro Glu
20 25 30
Leu Arg Cys Ala Thr Gly Glu Ala Trp Gln Asp Ile
35 40

<210> 42
<211> 44
<212> PRT
<213> Unknown

<220>
<223> Mammalian T-Type Ca Channel

<400> 42

Gln Val Ile Thr Leu Glu Gly Trp Val Asp Ile Gln Ile Leu Thr Gln
1 5 10 15
Glu Asp Trp Asn Lys Val Val Leu Ala Ser Lys Asp Gly Trp Val Asp
20 25 30
Ile Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile
35 40

<210> 43
<211> 44
<212> PRT
<213> Unknown

<220>
<223> Mammalian Na Channels

<400> 43
Arg Leu Met Thr Gln Asp Phe Trp Glu Asn Leu Arg Val Leu Cys Gly
1 5 10 15
Glu Trp Ile Glu Thr Met Gln Val Ala Thr Phe Lys Gly Trp Met Asp
20 25 30
Ile Gln Ile Thr Thr Ser Ala Gly Trp Asp Gly Leu
35 40

<210> 44
<211> 9
<212> PRT
<213> Unknown

<220>
<223> Consensus motif

a^b
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Gln Gln Glu Leu Gly Tyr Trp Ile Glu
1 5

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<210> 45
<211> 4
<212> PRT
<213> Unknown

<220>
<223> T-type channels in P-regions of domains I-IV

<400> 45
Glu Glu Asp Asp
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<210> 46
<211> 4
<212> PRT
<213> Unknown

<220>
<223> Na channels in the P-region of domains I-IV

<400> 46
Asp Glu Lys Ala
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<210> 47
<211> 4
<212> PRT
<213> Unknown

<220>
<223> L-type calcium channels in P-regions of domains
I-IV

<400> 47
Glu Glu Glu Glu
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<210> 48
<211> 18
<212> DNA
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<223> primer

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gcgtggagct ctttggag

18

<210> 49
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<400> 49
gcacccagtg gagaaaggtg

20